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Original Research Article

PREVALENCE OF MICROORGANISMS RESPONSIBLE FOR VULVOVAGINITIS AMONG PATIENTS PRESENTING TO A TERTIARY CARE HOSPITAL IN RIYADH, SAUDI ARABIA

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ABSTRACT

Background: Vulvovaginitis is a common gynecological condition resulting from disruption of the normal vaginal microbiota and the proliferation of pathogenic microorganisms. Accurate identification of the causative organism is necessary for appropriate treatment and may reduce unnecessary empirical antimicrobial therapy. **Objective:** To determine the prevalence and distribution of microorganisms responsible for vulvovaginitis among symptomatic non-pregnant women presenting to a tertiary care hospital in Riyadh, Saudi Arabia.

Materials and Methods: This retrospective cross-sectional study included high vaginal swab specimens collected from symptomatic non-pregnant women during the study period. Prepubertal and postmenopausal women were excluded. Women whose specimens were submitted only for Gram staining and assessment of bacterial vaginosis were also excluded. Demographic, parity, and microbiological data were retrieved from institutional records. Data were analyzed using IBM SPSS Statistics version 30. Categorical variables were presented as frequencies and percentages, and associations were assessed using the chi-square test, with a p-value <0.05 considered statistically significant.

Results: A total of 4,055 high vaginal swab specimens were evaluated, of which 1,690 (41.7%) were culture-positive. Among the positive specimens, 22 (1.3%) yielded more than one organism, resulting in the isolation of 1,712 microorganisms. Of the women with positive cultures, 851 (50.4%) were aged 18–28 years and 697 (41.2%) were aged 28.1–38 years. Most women had a parity of three or less (1,487/1,690; 88.0%). Candida albicans was the predominant isolate, accounting for 1,211 (70.7%) of all microorganisms, followed by non-albicans Candida species in 318 (18.6%) and other organisms in 183 (10.7%). Candida albicans and non-albicans Candida species were the most frequently identified organisms among women aged ≤38 years. Among the C. albicans isolates, 1,140 (94.1%) were recovered from women with a parity of three or less. Parity was significantly associated with the distribution of causative microorganisms (p=0.001). Among the non-candidal organisms, Streptococcus agalactiae and Escherichia coli were the most frequently isolated pathogens.

Conclusion: Candida albicans was the leading cause of vulvovaginitis, followed by non-albicans Candida species, across the studied age groups. Microbiological evaluation should be incorporated into the routine assessment of symptomatic women to identify the causative organism, guide targeted treatment, and reduce inappropriate empirical therapy.

Keywords: Vulvovaginitis, vulvovaginal candidiasis, Candida albicans, non-albicans Candida, vaginal infection.

INTRODUCTION

The vaginal microbiota comprises aerobic, anaerobic, and facultative anaerobic microorganisms that contribute to the maintenance of vaginal homeostasis and provide an important defense against pathogenic organisms. Disruption of this microbial balance may permit the overgrowth of pathogenic or opportunistic microorganisms, resulting in vulvovaginitis.[1] The composition of the vaginal microbiota is influenced by several behavioral and physiological factors, including sexual activity, number of sexual partners, phase of the menstrual cycle, immune status, age, and anatomical factors.[2]

Vulvovaginitis is among the most common genitourinary conditions encountered in gynecological practice. It is characterized by inflammation of the vulva and vagina, generally accompanied by symptoms such as abnormal vaginal discharge, pruritus, irritation, burning, and discomfort. In contrast, the term vaginosis refers to an alteration in the vaginal microbiota without a prominent inflammatory response.[3] Approximately 75% of women experience at least one episode of vulvovaginitis during their lifetime.[4] Gardnerella vaginalis, Candida species, and Trichomonas vaginalis have been reported among its most common infectious causes.[5]

Vulvovaginal candidiasis is considered the second most common vaginal infection after bacterial vaginosis and affects millions of women worldwide, creating a substantial clinical burden.[6] It commonly presents with vulvovaginal pruritus, burning, erythema, and a thick, curd-like vaginal discharge. Approximately 70% of women experience at least one episode of vulvovaginal candidiasis during their lifetime.[7] The condition is caused by yeasts of the genus Candida, with Candida albicans being the predominant species. Other implicated species include C. glabrata, C. tropicalis, and C. parapsilosis.[8]

Although C. albicans may exist as a commensal organism on the skin and within the gastrointestinal, reproductive, and urinary tracts, it can become pathogenic under favorable conditions, particularly in individuals with impaired host defenses.[9] Additional predisposing factors include recent or prolonged antibiotic use, pregnancy, diabetes mellitus, and immunosuppression.[10] Identifying the microorganisms associated with vulvovaginitis is essential for selecting appropriate treatment and reducing persistent or recurrent infection.

Therefore, the present study aimed to determine the prevalence and distribution of microorganisms associated with vulvovaginitis among nonpregnant women in the study population.

MATERIALS AND METHODS

This retrospective, hospital-based observational study was conducted at Dr Sulaiman Al Habib Hospital, Suwaidi, a tertiary care hospital in Riyadh, Saudi Arabia. Routinely collected clinical and microbiology laboratory records were reviewed for the period from September 1, 2023, to September 30, 2024. All eligible records identified during the predefined study period were included; therefore, no formal sample-size calculation was performed.

The study population comprised symptomatic women from whom high vaginal swabs were obtained as part of routine clinical care. Records were eligible if the patient was nonpregnant and premenopausal. Prepubertal, pregnant, and postmenopausal patients were excluded. Women evaluated for bacterial vaginosis using a separate Gram-stained vaginal specimen and Nugent score were also excluded because bacterial vaginosis was outside the microbiological scope of the study.

Eligible records were identified retrospectively from the hospital's clinical and microbiology laboratory databases. Extracted variables included culture result, number of organisms recovered, organism identification, patient age, and parity. Age was categorized as 18–28, 28.1–38, 38.1–48, and more than 48 years. Parity was categorized as 3 or less and 4 or more. Isolated microorganisms were classified as Candida albicans, non-albicans Candida species, or other organisms. Non-Candida organisms were additionally summarized by species or genus according to the available laboratory results.

The primary outcome was the distribution of microorganisms recovered from culture-positive high vaginal swabs. Secondary outcomes included the proportion of specimens showing microbial growth, the proportions with monomicrobial and polymicrobial growth, the distributions of age and parity, and the associations between age group, parity, and organism category. Monomicrobial growth was defined as the recovery of one organism from a specimen, whereas polymicrobial growth was defined as the recovery of more than one organism. Specimen-level denominators were used to report culture positivity and polymicrobial growth, while isolate-level denominators were used to describe the distribution of microorganisms.

High vaginal swabs were collected from symptomatic women during routine clinical care and processed in the hospital microbiology laboratory. Culture-positive results and organism identifications recorded in the laboratory information system were used in the analysis. Details of the collection device, transport medium, culture media, incubation conditions, organism-identification platform, manufacturer, and laboratory quality-control procedures should be added according to the protocol used by the hospital laboratory.

Data were analyzed using IBM SPSS Statistics for Windows, version 30.0 (IBM Corp., Armonk, NY, USA). Categorical variables were summarized as frequencies and percentages. Pearson's chi-square test was used to assess the association between age group and parity and the association between organism category and parity. Test statistics, degrees of freedom, and P values were reported. All statistical tests were two-sided, and $P < 0.05$ was considered statistically significant. Percentages were calculated using the denominator specified for each analysis and rounded to one decimal place.

RESULTS

During the study period, 4,055 high vaginal swab specimens obtained from symptomatic, nonpregnant premenopausal women were processed. Microbial growth was detected in 1,690 specimens (41.7%); the remaining 2,365 specimens (58.3%) showed no growth. Among the culture-positive specimens, 1,668 (98.7%) yielded a single organism and 22 (1.3%) yielded more than one organism, resulting in 1,712 isolates overall (Table 1)

Table 1. Culture results of high vaginal swab specimens (N = 4,055)

Culture result	n	%
No growth	2,365	58.3
Culture positive	1,690	41.7
Monomicrobial growth	1,668	98.7*
Polymicrobial growth	22	1.3*

*Percentage calculated using culture-positive specimens (n = 1,690) as the denominator

Of the 1,690 women with positive cultures, 851 (50.4%) were aged 18-28 years and 697 (41.2%) were aged 28.1-38 years; therefore, 91.6% of the study population was aged 38 years or younger. Overall, 1,487 women (88.0%) had a parity of 3 or less and 203 (12.0%) had a parity of 4 or more. Parity distribution differed significantly across age groups (chi-square statistic = 339.05, df = 3; $P < 0.001$) (Table 2).

Table 2. Age and parity distribution among women with positive cultures (N = 1,690)

Age group, years	Total, n (%)	Parity <=3, n (%)*	Parity >=4, n (%)*
18-28	851 (50.4)	828 (97.3)	23 (2.7)
28.1-38	697 (41.2)	596 (85.5)	101 (14.5)
38.1-48	124 (7.3)	59 (47.6)	65 (52.4)
>48	18 (1.1)	4 (22.2)	14 (77.8)
Total	1,690 (100.0)	1,487 (88.0)	203 (12.0)

Values are n (%) unless otherwise indicated. *Row percentages. Pearson chi-square statistic = 339.05; df = 3; $P < 0.001$.

Of the 1,712 isolates recovered, Candida albicans was the predominant organism (n = 1,211; 70.7%), followed by non-albicans Candida species (n = 318; 18.6%). Together, Candida species accounted for 1,529 isolates (89.3%). The remaining 183 isolates (10.7%) comprised other bacterial organisms (Table 3).

Table 3. Distribution of organisms isolated from positive cultures (N = 1,712 isolates)

Organism group	n	%
Candida albicans	1,211	70.7
Non-albicans Candida species	318	18.6
Other organisms	183	10.7
Total	1,712	100.0

The isolate denominator exceeds the specimen denominator because 22 specimens yielded polymicrobial growth.

The distribution of organism categories differed significantly by parity (chi-square statistic = 219.15, df = 2; $P < 0.001$). Candida albicans accounted for 76.7% of organism categories among women with parity 3 or less, whereas non-albicans Candida species accounted for 56.7% among women with parity 4 or more (Table 4).

Table 4. Organism category according to parity (N = 1,690 women)

Parity	C. albicans, n (%)*	Non-albicans Candida, n (%)*	Other organisms, n (%)*	Total, n (%)
<=3	1,140 (76.7)	203 (13.7)	144 (9.7)	1,487 (88.0)
>=4	71 (35.0)	115 (56.7)	17 (8.4)	203 (12.0)
Total	1,211 (71.7)	318 (18.8)	161 (9.5)	1,690 (100.0)

Values are n (%) unless otherwise indicated. *Row percentages. Mutually exclusive patient-level organism categories were used for this analysis; the additional isolates from polymicrobial specimens were not counted separately. Pearson chi-square statistic = 219.15; df = 2; $P < 0.001$.

Among the 183 non-Candida isolates, Streptococcus agalactiae was the most frequently identified organism (n = 87; 47.5%), followed by Escherichia coli (n = 48; 26.2%) and Klebsiella pneumoniae (n = 25; 13.7%) (Table 5).

Table 5. Distribution of non-Candida isolates (N = 183)

Organism	n	%
Streptococcus agalactiae	87	47.5
Escherichia coli	48	26.2
Klebsiella pneumoniae	25	13.7
Staphylococcus aureus	14	7.7
Klebsiella oxytoca	3	1.6
Acinetobacter species	2	1.1
Staphylococcus haemolyticus	2	1.1
Citrobacter species	1	0.5
Streptococcus pyogenes	1	0.5
Total	183	100.0

DISCUSSION

Candida species are among the most frequent causes of fungal infections and are also recognized as important healthcare-associated pathogens.[11] Candida albicans remains the predominant species isolated from human infections; however, a substantial increase in infections caused by non-albicans Candida (NAC) species has been reported over the past two decades.[12] Factors contributing to this changing epidemiological pattern include severe immunosuppression, prematurity, prolonged or empirical use of broad-spectrum antibiotics, and extensive exposure to antifungal agents. Although infections caused by different Candida species may have similar clinical presentations, several NAC species have reduced susceptibility or intrinsic resistance to commonly used antifungal drugs, making accurate species identification clinically important.[13]

Approximately 20% of premenopausal women may have asymptomatic vaginal colonization with Candida species, and this proportion may increase to nearly 30% during late pregnancy and among immunocompromised women. Several host-related factors, including impaired local defence mechanisms, genetic polymorphisms, allergic conditions, elevated serum glucose levels, antibiotic exposure, psychosocial stress, and increased oestrogen levels, may influence the development of vulvovaginal candidiasis (VVC). NAC species are responsible for approximately 10% of VVC cases. These infections may produce relatively mild symptoms, including premenstrual pruritus, vulvovaginal burning, erythema, and odourless vaginal discharge.[14] The frequency reported in the cited study was slightly lower than that observed in the present study, which may reflect differences in the characteristics of the study populations, diagnostic methods, patterns of antimicrobial exposure, and underlying host factors.

Most women experience at least one episode of VVC during their lifetime. Nevertheless, symptoms alone are insufficient for establishing the diagnosis because vaginal discharge, itching, burning, and irritation may also occur in bacterial, parasitic, inflammatory, or mixed vaginal infections. Antifungal treatment should therefore be prescribed for clinically and microbiologically confirmed cases. Fungal culture with species identification is particularly recommended in women with recurrent, persistent, or complicated VVC, as well as in those who do not respond to empirical therapy. In contrast, asymptomatic vaginal colonization generally does not require treatment, and routine treatment of an asymptomatic sexual partner is not recommended.[15]

Vulvovaginitis remains a clinically important problem because symptoms such as vaginal discharge, pain, irritation, and pruritus can substantially affect women's comfort and quality of life.[16] Vulvovaginitis has also been reported frequently among prepubertal and adolescent females;[17] however, these age groups were excluded from the present study in accordance with the eligibility criteria. The current findings indicated that typical physical signs were not consistently present among women with microbiologically confirmed infections. Moreover, empirical treatment was frequently inconsistent with the identified causative organism. These observations support the need for laboratory-based diagnosis rather than reliance on symptoms and physical examination alone. Similar findings were reported by Huang et al.,[18] who observed that clinical manifestations had limited diagnostic accuracy and that empirical management was often inappropriate.

In the present study, Candida species were the most frequently identified organisms among premenopausal women. This finding may be explained by the oestrogenized vaginal epithelium in women of reproductive age, which promotes glycogen accumulation and may facilitate the adherence and proliferation of Candida species. A comparable association was reported by Sheppard et al.,[19] who observed that vulvovaginal fungal infections were less common after menopause and occurred predominantly among postmenopausal women receiving hormone-replacement therapy. Overall, these findings emphasize the importance of considering reproductive and hormonal status when evaluating women with symptoms of vulvovaginitis.

CONCLUSION

The findings emphasize the importance of integrating clinical assessment with appropriate laboratory diagnostic tools to accurately identify the causative organism and improve the management of women presenting with vaginitis. Reliance on empirical treatment alone may lead to inappropriate therapy, particularly because Candida albicans and non-albicans Candida species were commonly detected across all age groups. Vulvovaginal infections were more prevalent among younger women aged 18–38 years. Further prospective, multicentre studies with larger sample sizes are recommended to confirm these findings and evaluate associated risk factors and antifungal susceptibility patterns.

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